

**AMENDMENTS TO THE CLAIMS**

1. (Currently Amended) A sample analyzing method, which comprises:

~~a step~~ (a) adding at least one reference material to each of multiple samples;

(b) obtaining three-dimensional data as a result of chromatography mass spectrometry for the multiple samples, wherein the three-dimensional data comprises a parameter indicating a mass-to-charge ratio, a parameter indicating ionic intensity, and a parameter indicating a retention time; of

~~(c) correcting the at least a one-dimensional parameter in multi~~ indicating a retention time in the three-dimensional data for the multiple samples using at least one peak of the at least one reference material; obtained as a result of the analysis of a sample; and

~~a step (b) of~~

(d) comparing the corrected data obtained in said step (c) a) for the multiple samples to analyze differences among the multiple samples; and

(e) outputting a result of the comparison in step (d).

2. (Canceled)

3. (Currently Amended) The sample analyzing method according to claim 1, wherein, in said step ~~(c), a)~~, profiles regarding parameters, from which a parameter as a correction target has been excluded, are used as reference profiles, and wherein using an evaluation function acting as a scale of position similarity regarding a plurality of reference profiles among multiple samples, the position of each profile is determined as a problem of finding an optimum solution which optimizes the value of said evaluation function.

4. (Original) The sample analyzing method according to claim 3, wherein said evaluation function is defined with one or more terms selected from the group consisting of the following terms (1) to (5):

(1) a term regarding similarity and/or distance among profiles regarding a parameter of a correction target;

(2) a term regarding similarity and/or distance among profiles regarding a reference profile;

(3) a term regarding the degree of concordance of data points among profiles as comparison targets;

(4) a term regarding the degree of discordance of data points among profiles as comparison targets;

(5) a term regarding the degree of concordance or discordance of reference material-derived signals among profiles as comparison targets; and

(6) a term regarding the degree of concordance in the previous comparison during repeated comparison operations.

5. (Currently amended) The sample analyzing method according to claim 3, wherein, in said step ~~(a)~~(c), dynamic programming algorithm is used, when the value of said evaluation function is optimized as a problem of finding an optimum solution regarding said parameter of a correction target.

6. (Original) The sample analyzing method according to claim 5, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, the score of a correspondence regarding data points derived from a reference material is set by a point-addition scoring system.

7. (Original) The sample analyzing method according to claim 5, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, a constraint condition is set, in which a correspondence regarding data points derived from a reference material is necessarily corresponded at a designated point.

8. (Currently Amended) The sample analyzing method according to claim 1, wherein said multiple sample comprise samples comprise a protein group and/or a peptide group.

9. (Canceled)

10. (Currently Amended) The sample analyzing method according to claim 1, 9, wherein said at least one reference material is at least one type of peptide selected from the group consisting of peptide T (Ala-Ser-Thr-Thr-Asn-Tyr-Thr)(**SEQ ID NO: 1**),  $\beta$ -casomorphin-7 (Tyr-Pro-Phe-Pro-Gly-Pro-Ile)(**SEQ ID NO: 2**), and a structural analog thereof.

11. (Currently Amended) The sample analyzing method according to claim 1, 9, wherein each of said at least one reference material is added to said multiple sample samples in a state where it is immobilized in gel.

12. (Currently Amended) A computer-readable medium on which is embodied a sample analyzing program comprising instructions which, when executed, cause for allowing a computer to execute:

a procedure (a) of inputting ~~multi~~ three-dimensional data obtained as a result of chromatography mass spectrometry for multiple samples to each of which at least one reference material has been added, wherein the three-dimensional data comprises a parameter indicating a mass-to-charge ratio, a parameter indicating ionic intensity, and a parameter indicating a retention time; the analysis of a sample;

a procedure (b) of correcting the data of at least a one-dimensional parameter indicating a retention time in the three-dimensional data for the multiple samples using at least one peak of the reference material; from among the inputted multi-dimensional data; and

a procedure (c) of comparing ~~multi-dimensional data including~~ the data corrected in said procedure (b) for the multiple samples to analyze differences among the multiple samples; and

a procedure (d) of outputting a result of the comparison in said procedure (c).

13. (Canceled)

14. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 12, wherein, in said procedure (b), profiles regarding parameters, from which a parameter as a correction target has been excluded, are used as reference profiles, and wherein using an evaluation function acting as a scale of position similarity regarding a plurality of reference profiles among multiple samples, the position of each profile is determined by optimizing the value of said evaluation function as a problem of finding an optimum solution.

15. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 14, wherein said evaluation function is defined with one or more terms selected from the group consisting of the following terms (1) to (5):

(1) a term regarding similarity and/or distance among profiles regarding a parameter of a correction target;

(2) a term regarding similarity and/or distance among profiles regarding a reference profile;

(3) a term regarding the degree of concordance of data points among profiles as comparison targets;

(4) a term regarding the degree of discordance of data points among profiles as comparison targets;

(5) a term regarding the degree of concordance or discordance of reference material-derived signals among profiles as comparison targets; and

(6) a term regarding the degree of concordance in the previous comparison during repeated comparison operations.

16. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 14, wherein, in said procedure (a), dynamic programming algorithm is used, when the value of said evaluation function is optimized as a problem of finding an optimum solution regarding said parameter of a correction target.

17. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 16, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, the score of a correspondence regarding data points derived from a reference material is set by a point-addition scoring system.

18. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 16, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, a constraint condition is set, in which a correspondence regarding data points derived from a reference material is necessarily corresponded at a designated point.

19. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 12, wherein said multiple samples comprise s-a protein group and/or a peptide group, and wherein multi-dimensional data derived from said protein group and/or peptide group are analyzed.

20. (Canceled)

21. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 12, 0, wherein said at least one reference material is at least one type of peptide selected from the group consisting of peptide T (Ala-Ser-Thr-Thr-Asn-Tyr-Thr)(**SEQ ID NO: 1**),  $\beta$ -casomorphin-7 (Tyr-Pro-Phe-Pro-Gly-Pro-Ile)(**SEQ ID NO: 2**), and a structural analog thereof.

22. (Currently Amended) The ~~sample-analyzing program~~ computer-readable medium according to claim 12, 0, wherein each of said at least one reference material is added to said multiple sample-samples in a state where it is immobilized in gel.